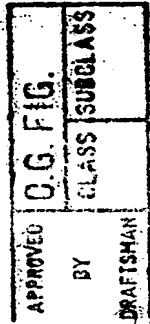




FIGURE 1A.1



ATG AAG CCG TAC TTC TGC CGT GTC TTT GTC TTC TGC TTC CTA ATC	45
M K P Y F C R V F V F C F L I	
5 10 15	
AGA CTT TTA ACA GGA GAA ATC AAT GGC TCG GCC GAT CAT AGG ATG	90
R L L T G *E I N G S A D H R M	
20 25 30	
TTT TCA TTT CAC AAT GGA GGT GTA CAG ATT TCT TGT AAA TAC CCT	135
F S F H N G G V Q I S C K Y P	
35 40 45	
GAG ACT GTC CAG CAG TTA AAA ATG CGA TTG TTC AGA GAG AGA GAA	180
E T V Q Q L K M R L F R E R E	
50 55 60	
GTC CTC TGC GAA CTC ACC AAG ACC AAG GGA AGC GGA AAT GCG GTG	225
V L C E L T K T K G S G N A V	
65 70 75	
TCC ATC AAG AAT CCA ATG CTC TGT CTA TAT CAT CTG TCA AAC AAC	270
S I K N P M L C L Y H L S N N	
80 85 90	
AGC GTC TCT TTT TTC CTA AAC AAC CCA GAC AGC TCC CAG GGA AGC	315
S V S F F L N N P D S S Q G S	
95 100 105	
TAT TAC TTC TGC AGC CTG TCC ATT TTT GAC CCA CCT CCT TTT CAA	360
Y Y F C S L S I F D P P P F Q	
110 115 120	
GAA AGG AAC CTT AGT GGA GGA TAT TTG CAT ATT TAT GAA TCC CAG	405
E R N L S G G Y L H I Y E S Q	
125 130 135	
CTC TGC TGC CAG CTG AAG CTC TGG CTA CCC GTA GGG TGT GCA GCT	450
L C C Q L K L W L P V G C A A	
140 145 150	
TTC GTT GTG GTA CTC CTT TTT GGA TGC ATA CTT ATC ATC TGG TTT	495
F V V V L L F G C I L I I W F	
155 160 165	
TCA AAA AAG AAA TAC GGA TCC AGT GTG CAT GAC CCT AAT AGT GAA	540
S K K K Y G S S V H D P N S E	
170 175 180	



FIGURE 1A.2

TAC	ATG	TTC	ATG	GCG	GCA	GTC	AAC	ACA	AAC	AAA	AAG	TCT	AGA	CTT	585
Y	M	F	M	A	A	V	N	T	N	K	K	S	R	L	
				185					190					195	
GCA GGT GTG ACC TCA															600
A	G	V	T	S											
				200											

APPROVED	O.G. FIG.	CLASS	SUBCLASS
BY			
DRAFTSMAN			



FIGURE 1B

mCRP1	MKPYFCRVFV	FCFLIRLL--	-----TGEIN	GS----	ADHR	MFSFHNGGVQ	39
mCD28	MT-----	----LRLFL	ALNFFSVQVT	ENKILVKQSP	LLVVDSNEVS		38
Consensus	M.....RLL..V.		
mCRP1	ISCKYPETV-	-QQLKMRLFR	--EREV-LCE	LTKTKGSGNA	VSIKNPMLCL		84
mCD28	LSCRYSYNLL	AKEFRASLYK	GVNSDVEVCV	GNGNFTYQPQ	FRSNAEFNCD		88
Consensus	.SC.Y.....L..V..C.C.		
mCRP1	YHLSNNSVSF	FLNPNDSQ	SYFCSLSIF	DPPPFQERNL	SGGYL-HIYE		133
mCD28	GDFDNETVTF	RLWNLHVNHT	DIYFCKIEFM	YPPPYLDNER	SNGTIIHIKE		138
ConsensusN..V.F	.L.N.....	..YFC.....	.PPP.....	S.G...HI.E		
mCRP1	SQLC---CQL	KL-W-LPVGC	AA-FVVVLLF	GCIL-IIWFS	KKKY----GS		172
mCD28	KHLCHTQSSP	KLFWALVVVA	GVLFCYGLLV	TVALCVIWTN	SRRNRLQVT		188
Consensus	..LC.....	KL.W.L.V..	...F...LL.	...L..IW..		
mCRP1	SVH-DPNSEY	MFMAAVNTNK	KSR-LAGVTS				200
mCD28	TMNMTPRRPG	LTRKPYQPYA	PARDFAAYRP				218
ConsensusP....R..A....	...			

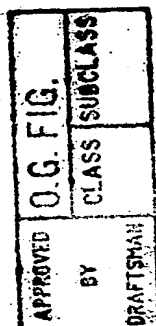




FIGURE 2A.1

ATG CAG CTA AAG TGT CCC TGT TTT GTG TCC TTG GGA ACC AGG CAG	45
M Q L K C P C F V S L G T R Q	
5 10 15	
CCT GTT TGG AAG AAG CTC CAT GTT TCT AGC GGG TTC TTT TCT GGT	90
P V W K K L H V S S G F F S G	
20 25 30	
CTT GGT CTG TTC TTG CTG CTG TTG AGC AGC CTC TGT GCT GCC TCT	135
L G L F L L L L S S L C A A S	
35 40 45	
GCA GAG ACT GAA GTC GGT GCA ATG GTG GGC AGC AAT GTG GTG CTC	180
A *E T E V G A M V G S N V V L	
50 55 60	
AGC TGC ATT GAC CCC CAC AGA CGC CAT TTC AAC TTG AGT GGT CTG	225
S C I D P H R R H F N L S G L	
65 70 75	
TAT GTC TAT TGG CAA ATC GAA AAC CCA GAA GTT TCG GTG ACT TAC	270
Y V Y W Q I E N P E V S V T Y	
80 85 90	
TAC CTG CCT TAC AAG TCT CCA GGG ATC AAT GTG GAC AGT TCC TAC	315
Y L P Y K S P G I N V D S S Y	
95 100 105	
AAG AAC AGG GGC CAT CTG TCC CTG GAC TCC ATG AAG CAG GGT AAC	360
K N R G H L S L D S M K Q G N	
110 115 120	
TTC TCT CTG TAC CTG AAG AAT GTC ACC CCT CAG GAT ACC CAG GAG	405
F S L Y L K N V T P Q D T Q E	
125 130 135	
TTC ACA TGC CGG GTA TTT ATG AAT ACA GCC ACA GAG TTA GTC AAG	450
F T C R V F M N T A T E L V K	
140 145 150	
ATC TTG GAA GAG GTG GTC AGG CTG CGT GTG GCA GCA AAC TTC AGT	495
I L E E V V R L R V A A N F S	
155 160 165	
ACA CCT GTC ATC AGC ACC TCT GAT AGC TCC AAC CCG GGC CAG GAA	540
T P V I S T S D S S N P G Q E	
170 175 180	

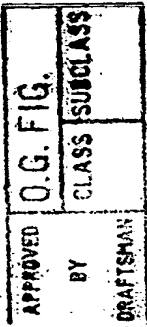




FIGURE 2A.2

CGT ACC TAC ACC TGC ATG TCC AAG AAT GGC TAC CCA GAG CCC AAC	585
R T Y T C M S K N G Y P E P N	
185 190 195	
CTG TAT TGG ATC AAC ACA ACG GAC AAT AGC CTA ATA GAC ACG GCT	630
L Y W I N T T D N S L I D T A	
200 205 210	
CTG CAG AAT AAC ACT GTC TAC TTG AAC AAG TTG GGC CTG TAT GAT	675
L Q N N T V Y L N K L G L Y D	
215 220 225	
GTA ATC AGC ACA TTA AGG CTC CCT TGG ACA TCT CGT GGG GAT GTT	720
V I S T L R L P W T S R G D V	
230 235 240	
CTG TGC TGC GTA GAG AAT GTG GCT CTC CAC CAG AAC ATC ACT AGC	765
L C C V E N V A L H Q N I T S	
245 250 255	
ATT AGC CAG GCA GAA AGT TTC ACT GGA AAT AAC ACA AAG AAC CCA	810
I S Q A E S F T G N N T K N P	
260 265 270	
CAG GAA ACC CAC AAT AAT GAG TTA AAA GTC CTT GTC CCC GTC CTT	855
Q E T H N N E L K V L V P V L	
275 280 285	
GCT GTA CTG GCG GCA GCG GCA TTC GTT TCC TTC ATC ATA TAC AGA	900
A V L A A A A F V S F I I Y R	
290 295 300	
CGC ACG CGT CCC CAC CGA AGC TAT ACA GGA CCC AAG ACT GTA CAG	945
R T R P H R S Y T G P K T V Q	
305 310 315	
CTT GAA CTT ACA GAC CAC GCC	966
L E L T D H A	
320 322	

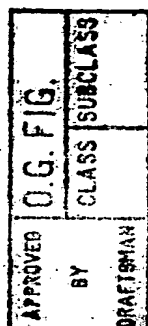




FIGURE 2B

APPROVED	BY	CRAFTSMAN	O.G. FIG.	
			CLASS	SUBCLASS

mB7RP1	MQLKPCPCFVS	LGTRQPVWKK	LHVSSGFFSG	LGLFLLLLS-	SLCAASAETE	49
mCD80	MA--CNC--Q	LMQDTPL---	LKFPCCPRI-	L-LFVLLIRL	SQVSSDVDEO	41
Consensus	M...C.C...	L....P....	L.....	L.LF.LL...	S.....	
mB7RP1	VGAMVGSNNV	LSCIDPHRRH	FNLSGLYVYW	QIENPEVSVT	YYLPYKSPGI	99
mCD80	LSKSVKDKVL	LPC-RYNsph	EDESEDRIYW	QKHDKVV---	--LSVIAGKL	85
ConsensusV...V.	L.C.....	H...S....Y	W.Q.....	V...L.....	
mB7RP1	NVDSSYKNRG	HLSLDSMKQG	NFSLYLKNVT	PQDTQEFTCR	VFMNTATELV	149
mCD80	KVWPEYKNR-	--TL--YDNT	TYSLIILGLV	LSDRGTYSKV	VQKKERGTYE	130
Consensus	.V...YKNR.	...L.....	..SL.....	..D.....	C.V.....	
mB7RP1	KILEEVVRLR	VAANFSTPVI	STSDSSNPGQ	ERTYTCMSKN	GYPEPNLYWI	199
mCD80	VKHLALVKLS	IKADFSTPNI	TESGNPSADT	KRI-TCFASG	GFPKPRFSWL	179
ConsensusV.L.	..A.FSTP.I	..S.....	.R..TC....	G.P.P...W.	
mB7RP1	-NTTDNSLID	TALQNNTVYL	NKLGLYDVIS	TLRLPWTSRG	DVLCCVENVA	248
mCD80	ENGRELPGIN	TTISQDPESE	LYTISSQLDF	NTTRNHTIKC	LIKYGDAHVS	229
Consensus	.N.....I.	T.....T...V.	
mB7RP1	LHQNITSISQ	AESFTGNNTK	NPQETHNNEL	KVLVPVLAVL	A-AAAFVSFI	297
mCD80	EDFTWEKPPE	DPPDSKNTLV	LFGAGFGAVI	TVVVIVVVIK	CFCKHRSCFR	279
ConsensusN...V.V.V....F.	
mB7RP1	IYRRTR-PHR	SYT-GPKTVQ	LELTDHA			322
mCD80	RNEASRETN	SLTFGPPEAL	AEQTVFL			306
ConsensusR....	S.T.GP....	.E.T...			



FIGURE 3A.1

O.G. FIG.	
APPROVED	BY
CLASS SUBCLASS	
DRAFTSMAN	

ATG CGG CTG GGC AGT CCT GGA CTG CTC TTC CTG CTC TTC AGC AGC	45
M R L G S P G L L F L L F S S	
5 10 15	
CTT CGA GCT GAT ACT CAG GAG AAG GAA GTC AGA GCG ATG GTA GGC	90
L R A *D *T *Q *E K *E V R A *M V G	
20 25 30	
AGC GAC GTG GAG CTC AGC TGC GCT TGC CCT GAA GGA AGC CGT TTT	135
S D V E L S C A C P E G S R F	
35 40 45	
GAT TTA AAT GAT GTT TAC GTA TAT TGG CAA ACC AGT GAG TCG AAA	180
D L N D V Y V Y W Q T S E S K	
50 55 60	
ACC GTG GTG ACC TAC CAC ATC CCA CAG AAC AGC TCC TTG GAA AAC	225
T V V T Y H I P Q N S S L E N	
65 70 75	
GTG GAC AGC CGC TAC CGG AAC CGA GCC CTG ATG TCA CCG GCC GGC	270
V D S R Y R N R A L M S P A G	
80 85 90	
ATG CTG CGG GGC GAC TTC TCC CTG CGC TTG TTC AAC GTC ACC CCC	315
M L R G D F S L R L F N V T P	
95 100 105	
CAG GAC GAG CAG AAG TTT CAC TGC CTG GTG TTG AGC CAA TCC CTG	360
Q D E Q K F H C L V L S Q S L	
110 115 120	
GGA TTC CAG GAG GTT TTG AGC GTT GAG GTT ACA CTG CAT GTG GCA	405
G F Q E V L S V E V T L H V A	
125 130 135	
GCA AAC TTC AGC GTG CCC GTC GTC AGC GCC CCC CAC AGC CCC TCC	450
A N F S V P V V S A P H S P S	
140 145 150	
CAG GAT GAG CTC ACC TTC ACG TGT ACA TCC ATA AAC GGC TAC CCC	495
Q D E L T F T C T S I N G Y P	
155 160 165	
AGG CCC AAC GTG TAC TGG ATC AAT AAG ACG GAC AAC AGC CTG CTG	540
R P N V Y W I N K T D N S L L	
170 175 180	



FIGURE 3A.2

GAC CAG GCT CTG CAG AAT GAC ACC GTC TTC TTG AAC ATG CGG GGC	585
D Q A L Q N D T V F L N M R G	
185 190 195	
TTG TAT GAC GTG GTC AGC GTG CTG AGG ATC GCA CGG ACC CCC AGC	630
L Y D V V S V L R I A R T P S	
200 205 210	
GTG AAC ATT GGC TGC TGC ATA GAG AAC GTG CTT CTG CAG CAG AAC	675
V N I G C C I E N V L L Q Q N	
215 220 225	
CTG ACT GTC GGC AGC CAG ACA GGA AAT GAC ATC GGA GAG AGA GAC	720
L T V G S Q T G N D I G E R D	
230 235 240	
AAG ATC ACA GAG AAT CCA GTC AGT ACC GGC GAG AAA AAC GCG GCC	765
K I T E N P V S T G E K N A A	
245 250 255	
ACG TGG AGC ATC CTG GCT GTC CTG TGC CTG CTT GTG GTC GTG GCG	810
T W S I L A V L C L L V V V A	
260 265 270	
GTG GCC ATA GGC TGG GTG TGC AGG GAC CGA TGC CTC CAA CAC AGC	855
V A I G W V C R D R C L Q H S	
275 280 285	
TAT GCA GGT	864
Y A G	
288	

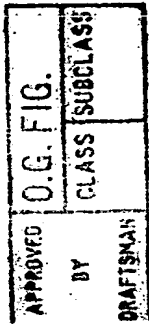
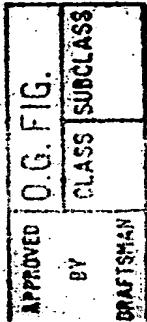




FIGURE 3B

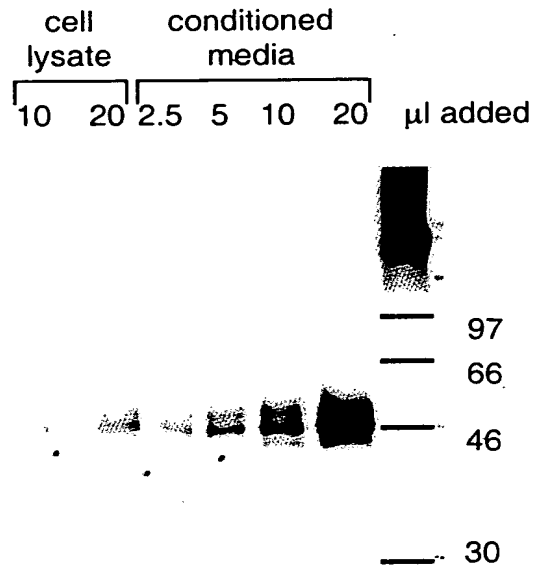
hB7RP1	EKEVRAMVGS	DVELSCACPE	GSRFDLNDVY	VYWQTSESKT	VVTYHIPQNS	50
mB7RP1	ETEVGAMVGS	NVVLSCIDPH	RRHFNLSGLY	VYWQIENPEV	SVTYLPLPKS	50
Consensus	E.EV.AMVGS	.V.LSC..P.	...F.L...Y	VYWQ.....	.VTY..P..S	
hB7RP1	SLENVDSRYR	NRALMSPAGM	LRGDFSLRLF	NVTPQDEQKF	HCLVLSQ-SL	99
mB7RP1	PGINVDSYK	NRGHLSLDSM	KQGNFSLYLK	NVTPQDTQEF	TCRVFMNTAT	100
Consensus	...NVDS.Y.	NR...S...M	..G.FSL.L.	NVTPQD.Q.F	.C.V.....	
hB7RP1	GFQEVLSVEV	TLHVAANFSV	PVVSAPHSPS	Q-DELTFTCT	SINGYPRPNV	148
mB7RP1	ELVKILEEVV	RLRVAANFST	PVISTSDSSN	PGQERTYTCM	SKNGYPEPNL	150
ConsensusL...V	.L.VAANFS.	PV.S...S..	...E..T.TC.	S..NGYP..PN.	
hB7RP1	YWINKTDNSL	LDQALQNDTV	FLNMRGLYDV	VSVLRIARTP	SVNIGCCCIEN	198
mB7RP1	YWINTTDNSL	IDTALQNNVT	YLNKLGLYDV	ISTLRPPTS	RGDVLCCVEN	200
Consensus	YWIN.TDNSL	.D.ALQN.TV	.LN..GLYDV	.S.LR...T.CC.EN	
hB7RP1	VLLQQNLTVG	SQTGNDIGER	DKITENPVST	GEKNAATWSI	LAVLCLLVVV	248
mB7RP1	VALHQNITSI	SQAESFTGNN	TKNPQETHNN	ELKVLV--PV	LAVLAAAFV	248
Consensus	V.L.QN.T..	SQ.....G..	.K.....	..K.....	LAVL.....V	
hB7RP1	AVAIGWVCRD	RCLQHSYAG				267
mB7RP1	SFIIYR--RT	R-PHRSYTGP	KTVQLELTDH	A		276
Consensus	...I....R.	R....SY.G.			





APPROVED	O.G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

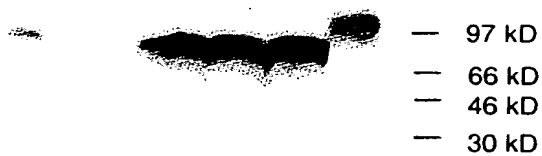
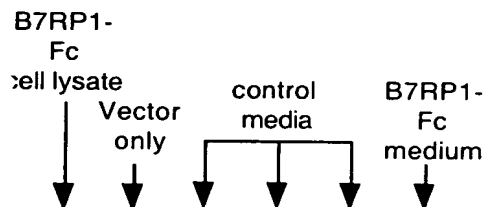
FIG. 4A





APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

FIG. 4B





APPROVED	O.G. FIG.	CLASS	SUBCLASS
BY			
DRAFTSMAN			

FIG. 5

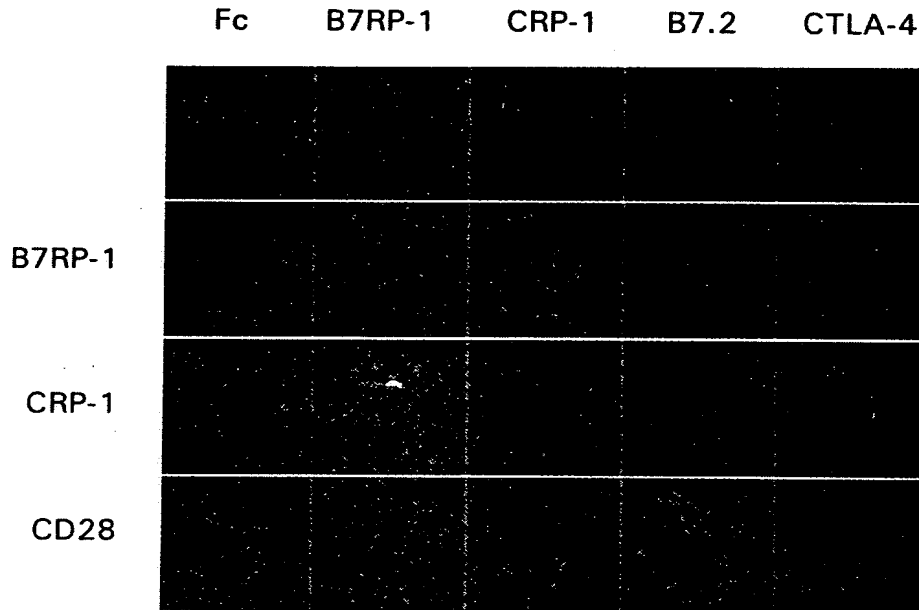




FIG. 6A

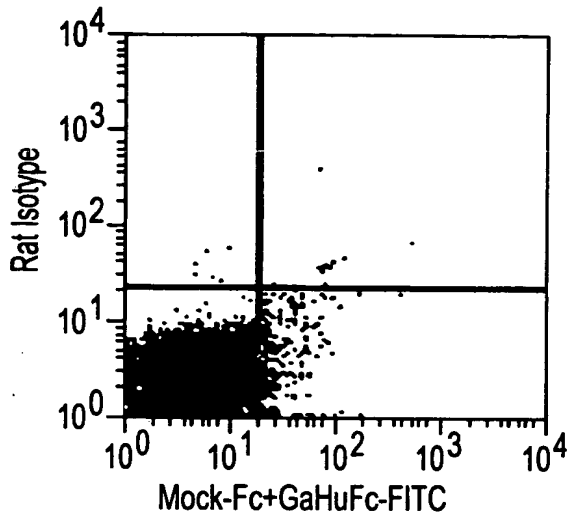


FIG. 6B

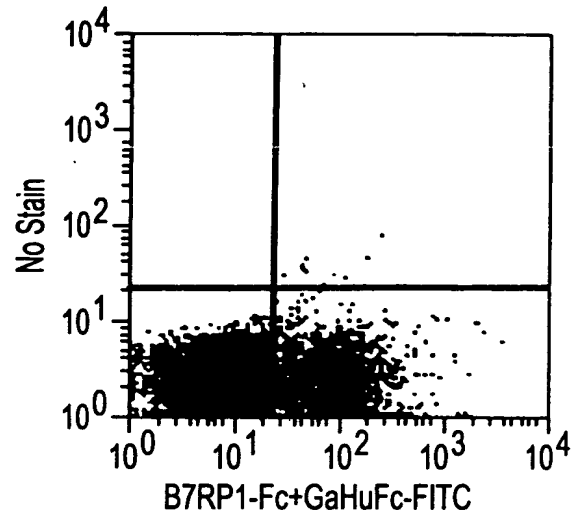


FIG. 6C

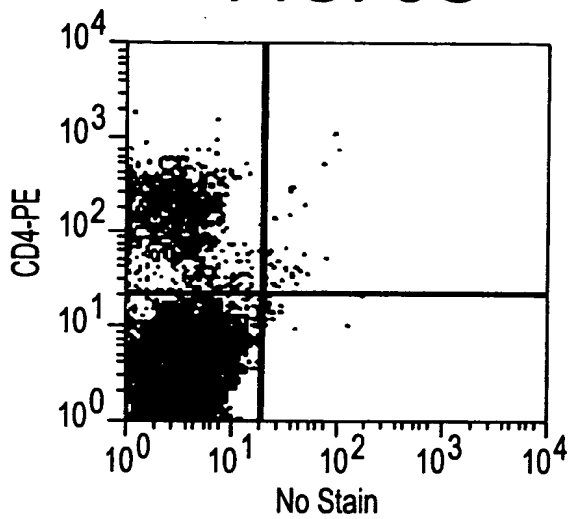


FIG. 6D

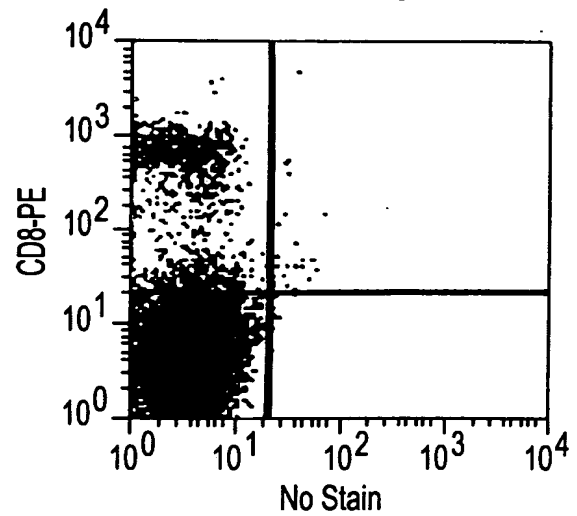


FIG. 6E

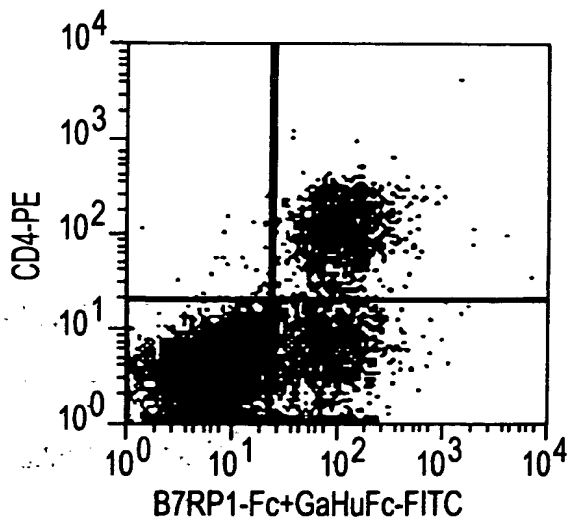
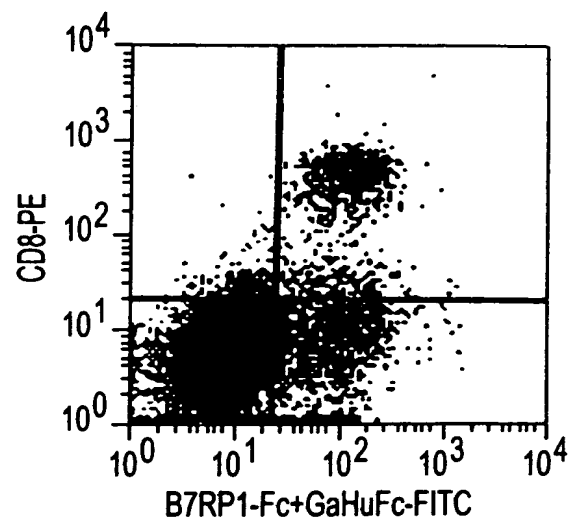


FIG. 6F



O.G. FIG.	
APPROVED	BY CLASS SUBCLASS
DRAFTSMAN	



O.G. FIG.	
APPROVED	BY
CLASS SUBCLASS	
DRAFTSMAN	

FIG. 7A

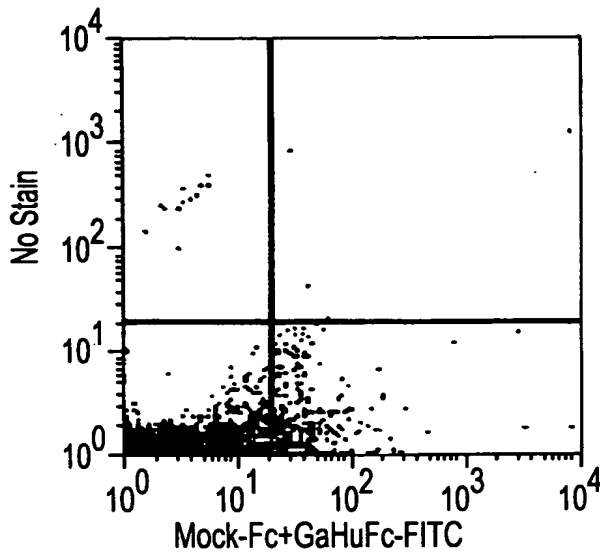


FIG. 7B

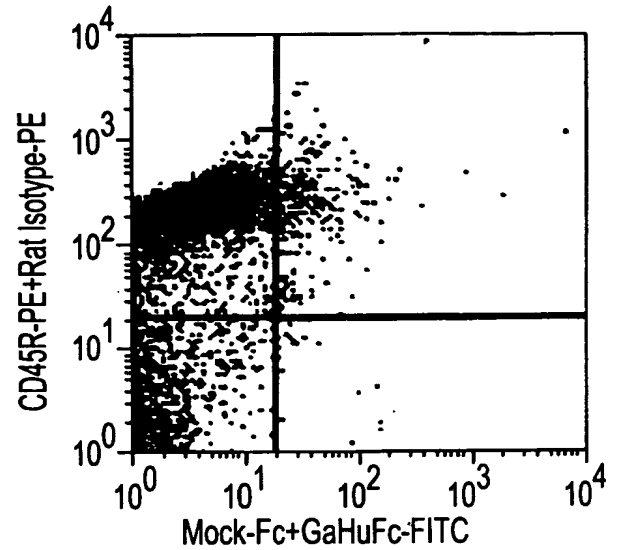
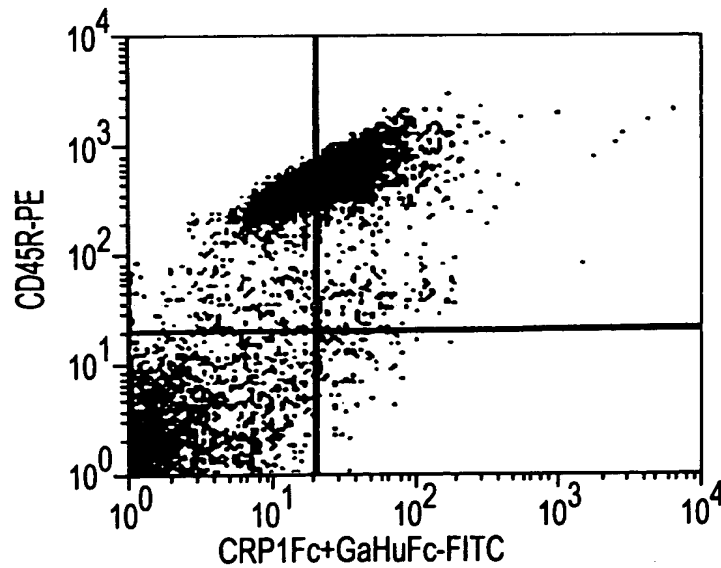


FIG. 7C





O.G. FIG.	
APPROVED	BY CLASS SUBCLASS
DRAFTSMAN	

FIG. 8A

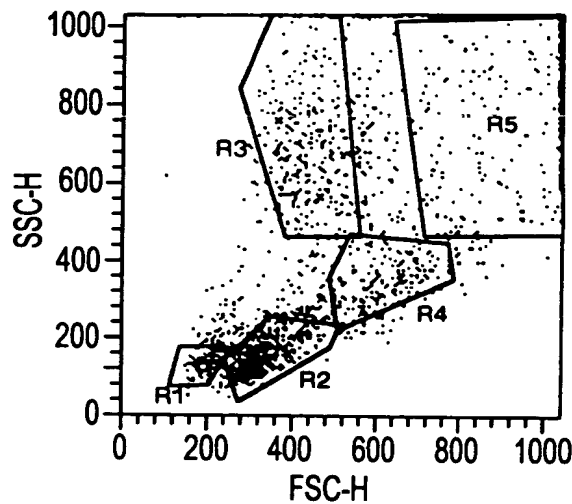


FIG. 8B

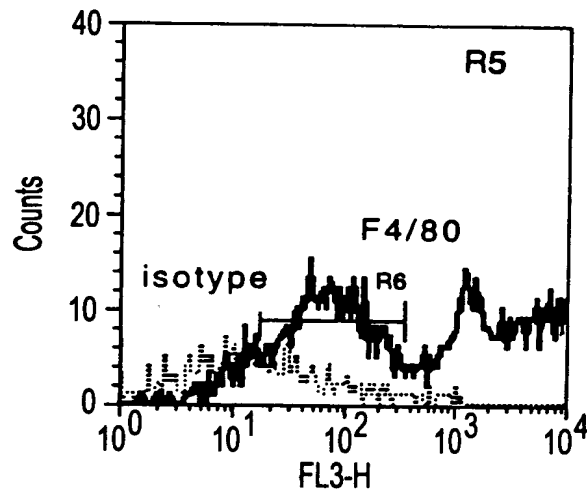
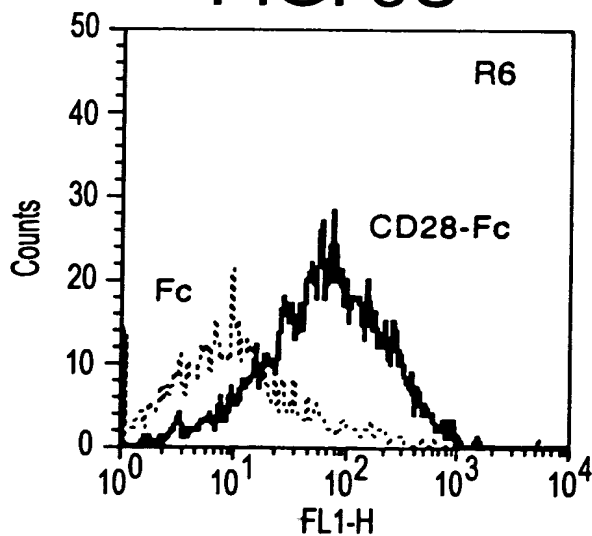


FIG. 8C





APPROVED	BY	CLASS	SUBCLASS
O.G. FIG.			
CRAFTSMAN			

FIG. 9

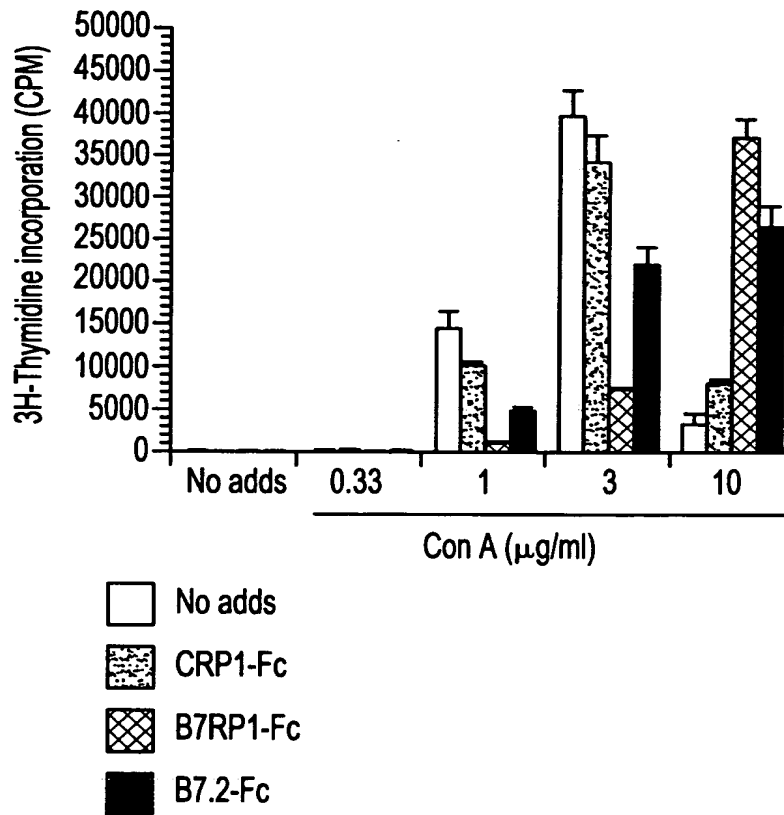




FIG. 10A

Lymph node-control#10

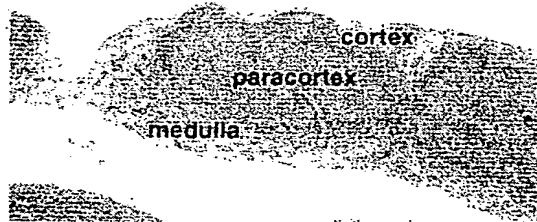


FIG. 10B

LN-WX11#40

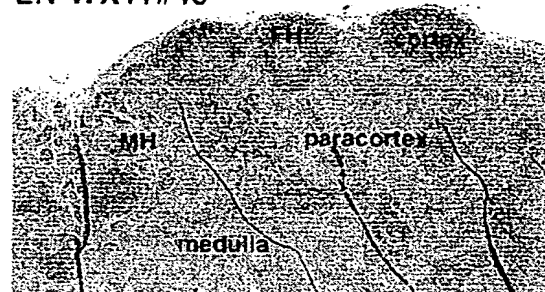


FIG. 10C

LN closeup-control#10

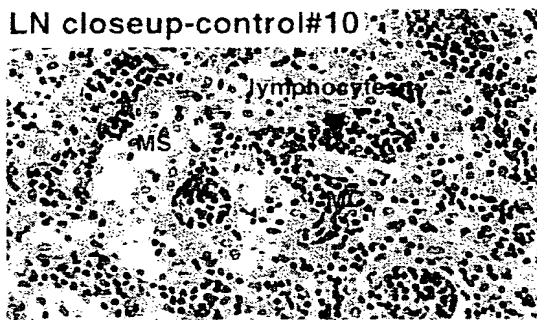


FIG. 10D

LN closeup-WX11#40

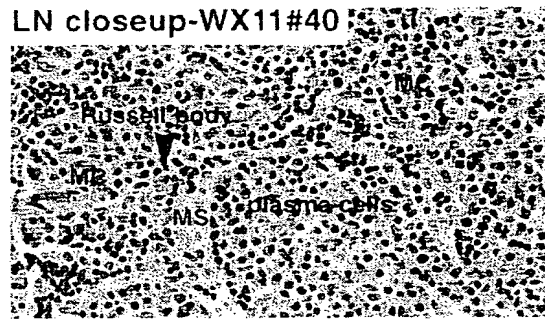


FIG. 10E

Spleen-control#10

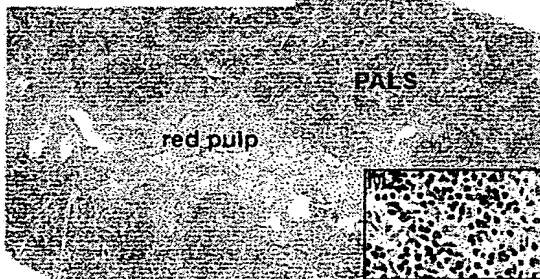


FIG. 10F

Spleen-WX11#6

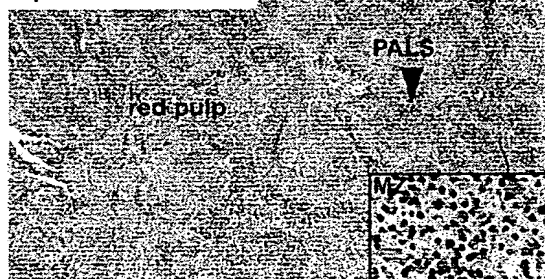


FIG. 10G

Ileum-control#25

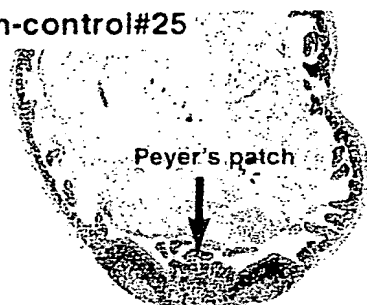


FIG. 10H

Ileum-WX11#32

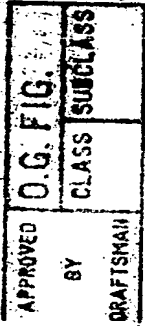
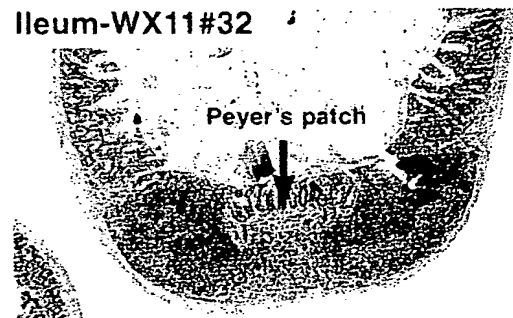




FIG. 11A



Control#5-H&E

FIG. 11B

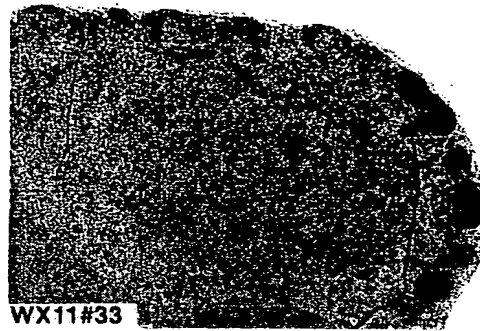


FIG. 11C



Control-B220 (B cells)

FIG. 11D



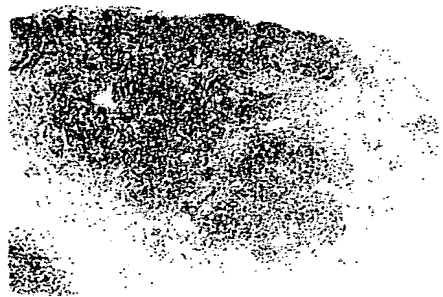
WX11-B220

FIG. 11E



Control-CD3 (T cells)

FIG. 11F



WX11-CD3

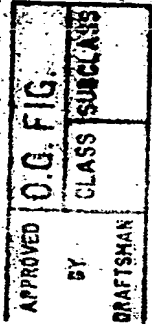
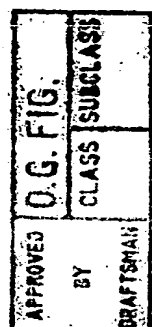




FIGURE 12A.1



GCTGGTACGCCTGCAGGTACCGGTCCGGAATTCCCGGGTCGACCCACGCGTCCGCCCACGCG -138
TCCGCGGGAGCGCAGTTAGAGCCGATCTCCCGCGCCCCGAGGTGCTCCTCTCCGAGGTCTC -76
CCGCGGCCCCAAGTTCTCCGCGCCCCGAGGTCTCCGCGCCCCGAGGTCTCCGCGCCCCGAGGT -14
CTCCGCCCCGACC -1

ATG CGG CTG GGC AGT CCT GGA CTG CTC TTC CTG CTC TTC AGC AGC 45
M R L G S P G L L F L L F S S
5 10 15

CTT CGA GCT GAT ACT CAG GAG AAG GAA GTC AGA GCG ATG GTA GGC 90
L R A *D *T *Q *E K *E V R A *M V G
20 25 30

AGC GAC GTG GAG CTC AGC TGC GCT TGC CCT GAA GGA AGC CGT TTT 135
S D V E L S C A C P E G S R F
35 40 45

GAT TTA AAT GAT GTT TAC GTA TAT TGG CAA ACC AGT GAG TCG AAA 180
D L N D V Y V Y W Q T S E S K
50 55 60

ACC GTG GTG ACC TAC CAC ATC CCA CAG AAC AGC TCC TTG GAA AAC 225
T V V T Y H I P Q N S S L E N
65 70 75

GTG GAC AGC CGC TAC CGG AAC CGA GCC CTG ATG TCA CCG GCC GGC 270
V D S R Y R N R A L M S P A G
80 85 90

ATG CTG CGG GGC GAC TTC TCC CTG CGC TTG TTC AAC GTC ACC CCC 315
M L R G D F S L R L F N V T P
95 100 105

CAG GAC GAG CAG AAG TTT CAC TGC CTG GTG TTG AGC CAA TCC CTG 360
Q D E Q K F H C L V L S Q S L
110 115 120

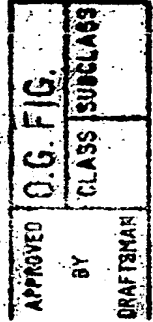
GGA TTC CAG GAG GTT TTG AGC GTT GAG GTT ACA CTG CAT GTG GCA 405
G F Q E V L S V E V T L H V A
125 130 135

GCA AAC TTC AGC GTG CCC GTC GTC AGC GCC CCC CAC AGC CCC TCC 450
A N F S V P V V S A P H S P S
140 145 150

CAG GAT GAG CTC ACC TTC ACG TGT ACA TCC ATA AAC GGC TAC CCC 495
Q D E L T F T C T S I N G Y P
155 160 165



FIGURE 12A.2



AGG CCC AAC GTG TAC TGG ATC AAT AAG ACG GAC AAC AGC CTG CTG 540
R P N V Y W I N K T D N S L L
170 175 180

GAC CAG GCT CTG CAG AAT GAC ACC GTC TTC TTG AAC ATG CGG GGC 585
D Q A L Q N D T V F L N M R G
185 190 195

TTG TAT GAC GTG GTC AGC GTG CTG AGG ATC GCA CGG ACC CCC AGC 630
L Y D V V S V L R I A R T P S
200 205 210

GTG AAC ATT GGC TGC TGC ATA GAG AAC GTG CTT CTG CAG CAG AAC 675
V N I G C C I E N V L L Q Q N
215 220 225

CTG ACT GTC GGC AGC CAG ACA GGA AAT GAC ATC GGA GAG AGA GAC 720
L T V G S Q T G N D I G E R D
230 235 240

AAG ATC ACA GAG AAT CCA GTC AGT ACC GGC GAG AAA AAC GCG GCC 765
K I T E N P V S T G E K N A A
245 250 255

ACG TGG AGC ATC CTG GCT GTC CTG TGC CTG CTT GTG GTC GTG GCG 810
T W S I L A V L C L L V V V A
260 265 270

GTG GCC ATA GGC TGG GTG TGC AGG GAC CGA TGC CTC CAA CAC AGC 855
V A I G W V C R D R C L Q H S
275 280 285

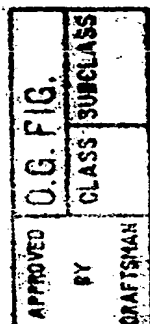
TAT GCA GGT GCC TGG GCT GTG AGT CCG GAG ACA GAG CTC ACT GGC 900
Y A G A W A V S P E T E L T G
300

CAC GTT TGA 909
H V STOP
302

CCGGAGCTCACC GCCCAGAGCGTGGACAGGGCTTCCGTGAGACGCCACCGTGAGAGGCCAGG 971
TGGCAGCTTGAGCATGGACTCCCAGACTGCAGGGGAGCACTTGGGGCAGCCCCAGAAGGAC 1033
CACTGCTGGATCCCAGGGAGAACCTGCTGGCGTTGGCTGTGATCCTGGAATGAGGCCCTTTC 1095



FIGURE 12B



human	MRLGSP----	-----G	L-LF-LLFSS	LRADTQEKEV	25	
mouse	MQLKPCPFVS	LGTRQPVWKK	LHVSSGFFSG	LGLFLLLLSS	LCAASAETEV	50
Consensus	M.L..P....G	L.LF.LL.SS	L.A...E.EV	50	
human	RAMVGSDEL	SCACPEGSRF	DLNDVYVYWQ	TSESKTVVTY	HIPQNSSLEN	75
mouse	GAMVGSNVVL	SCIDPHRRHF	NLSGLYVYWQ	IENPEVSVTY	YLPYKSPGIN	100
Consensus	.AMVGS.V.L	SC..P....F	.L...YVYWQVTY	..P..S...N	100
human	VDSRYRNRAL	MSPAGMLRGD	FSLRLFNVT	QDEQKFHCLV	LSQ-SLGFQE	124
mouse	VDSSYKNRGH	LSLDSMKQGN	FSLYLKINVTP	QDTQEFTCRV	FMNTATELVK	150
Consensus	VDS.Y.NR..	.S...M..G.	FSL.L.NVTP	QD.Q.F.C.V	150
human	VLSVEVTLHV	AANFSVPVVS	APHSPSQ-DE	LTFTCTSING	YPRPNVYWIN	173
mouse	ILEEVVRLRV	AANFSTPVIS	TSDSSNPGQE	RTYTCMSKNG	YPEPNLYWIN	200
Consensus	.L...V.L.V	AANFS.PV.S	...S.....E	.T.TC.S.NG	YP.PN.YWIN	200
human	KTDNSLLDQA	LQNDTVFLNM	RGLYDVVSVL	RIARTPSVNI	GCCIENVLLQ	223
mouse	TTDNSLIDTA	LQNNTVYLNK	LGLYDVISTL	RLPWTSRGDV	LCCVENVALH	250
Consensus	.TDNSL.D.A	LQN.TV.LN.	.GLYDV.S.L	R...T.....	.CC.ENV.L.	250
human	QNLTVGSQTG	NDIGERDKIT	ENPVSTGEKN	AATWSILAVL	CLLVVVAVAI	273
mouse	QNITSISQAE	SFTGNNTKNP	QETHNNELKV	LV--PVLAVL	AAAFVSFII	298
Consensus	QN.T..SQ..	...G...K..K.LAVLV...I	300
human	GWVCRDRCLQ	HSYAGAWAVS	PETELTGHV			302
mouse	YR--RTR-PH	RSYTGPKTVQ	LE--LTDHA			322
ConsensusR.R...	.SY.G...V.	.E..LT.H.			329

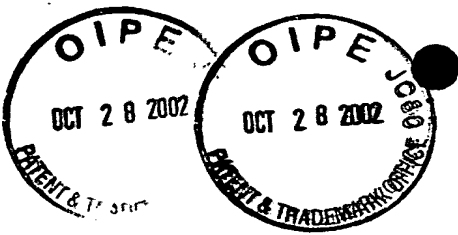


FIGURE 13A.1

APPROVED	BY	DRAFTSMAN	O.G. FIG.
			CLASS SUBCLASS

AACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAAGCTCTAATACGA	-111
CTCACTATAGGGAAAGCTGGTACGCCTGCAGGTACCGGTCCGGAATCCCGGGTC	-56
GACCCACGCGTCCGTGAACACTGAACGCGAGGACTGTAACTGTTTCTGGCAAAC	-1
ATG AAG TCA GGC CTC TGG TAT TTC TTT CTC TTC TGC TTG CGC ATT	45
M K S G L W Y F F L F C L R I	
5 10 15	
AAA GTT TTA ACA GGA GAA ATC AAT GGT TCT GCC AAT TAT GAG ATG	90
K V L T *G *E I N G S A N Y E M	
20 25 30	
TTT ATA TTT CAC AAC GGA GGT GTA CAA ATT TTA TGC AAA TAT CCT	135
F I F H N G G V Q I L C K Y P	
35 40 45	
GAC ATT GTC CAG CAA TTT AAA ATG CAG TTG CTG AAA GGG GGG CAA	180
D I V Q Q F K M Q L L K G G Q	
50 55 60	
ATA CTC TGC GAT CTC ACT AAG ACA AAA GGA AGT GGA AAC ACA GTG	225
I L C D L T K T K G S G N T V	
65 70 75	
TCC ATT AAG AGT CTG AAA TTC TGC CAT TCT CAG TTA TCC AAC AAC	270
S I K S L K F C H S Q L S N N	
80 85 90	
AGT GTC TCT TTT TTT CTA TAC AAC TTG GAC CAT TCT CAT GCC AAC	315
S V S F F L Y N L D H S H A N	
95 100 105	
TAT TAC TTC TGC AAC CTA TCA ATT TTT GAT CCT CCT CCT TTT AAA	360
Y Y F C N L S I F D P P P F K	
110 115 120	
GTA ACT CTT ACA GGA GGA TAT TTG CAT ATT TAT GAA TCA CAA CTT	405
V T L T G G Y L H I Y E S Q L	
125 130 135	
TGT TGC CAG CTG AAG TTC TGG TTA CCC ATA GGA TGT GCA GCC TTT	450
C C Q L K F W L P I G C A A F	
140 145 150	
GTT GTA GTC TGC ATT TTG GGA TGC ATA CTT ATT TGT TGG CTT ACA	495
V V V C I L G C I L I C W L T	
155 160 165	



FIGURE 13A.2

APPROVED	BY	DRAFTSMAN	O.G. FIG.	CLASS	SUBCLASS

AAA	AAG	AAG	TAT	TCA	TCC	AGT	GTG	CAC	GAC	CCT	AAC	GGT	GAA	TAC	540
K	K	K	Y	S	S	S	V	H	D	P	N	G	E	Y	
				170					175					180	

ATG	TTC	ATG	AGA	GCA	GTG	AAC	ACA	GCC	AAA	AAA	TCT	AGA	CTC	ACA	585
M	F	M	R	A	V	N	T	A	K	K	S	R	L	T	
				185					190					195	

GAT	GTG	ACC	CTA	TAA											600
D	V	T	L	STOP											
				199											

TATGGA	ACTCTGGC	ACCCAGGC	ATGAAG	CACGTTGGCC	CAGTTTTCTCA	ACTTGA	655
AGTGCA	AAGATTCTCT	TATTTCCGGG	ACCACGGAG	AGTCTGACTTAA	CTACATACA	710	
TCTTCT	GCTGGTGTTT	TGTTCAATCTGGA	AGAATGACTGTAT	CAGTCAATGGGGA	765		
TTTTAA	CAGACTGCCT	TGGTACTGCCGAG	TCTCTCAAAACAA	ACCCCTCTTGC	820		
AACCAG	CTTTGGAGAA	AGCCCAGCTCCT	GTGTGCTCACTGGG	AGTGGAATCCCTG	875		
TCTCCAC	ATCTGCTCCTAG	CAGTGCATCAGCC	AGTAAAACAAAC	CATTTACAAG	930		
AAAAAT	GTTTTTAAAG	ATGCCAGGGTACT	GAAATCTGCAAAG	CAAATGAGCAGCCA	985		
AGGACC	AGCATCTGTCCG	CATTTCACTATCATA	CTACTACCTCTTCT	TTTCTGTAGGGA	1040		
TGAGAAT	TCTCTTTTAA	TCAGTCAAGGGAG	ATGCTTCAAAGCT	GGAGCTATTTT	1095		
ATTTCT	GAGATGTTGAT	GTGAACTGTACAT	TAGTACATACTCAG	TACTCTCCTTC	1150		
AATTGCT	GAAACCCAGTT	GACCATTTTACCA	AGACTTTAGATGCT	TTCTTGTGCC	1205		



FIGURE 13B

O.G. FIG.	
APPROVED	BY
DRAFTSMAN	
CLASS	SUBCLASS

hCRP1	MKSGWLWYFFLFCLRIKVLTTGEINGSANYEMFIFHNGGVQILCKYPDIVQQ	50
mCRP1	. :. : :	50
hCRP1	MKPYFCRVFVFCFLIRLLTGEINGSADHRMFSFHNGGVQISCKYPETVQQ	50
hCRP1	FKMQLLKGGQILCDLTCTKGSGNTVSIKSLKFCHSQLSNNSVSFFLYNLD	100
mCRP1	. : : .	100
hCRP1	LKMRLFREREVLCELCTKTGSGNAVSIKNPMLCLYHLSNNSVSFFLNNPD	100
hCRP1	HSHANYFFCNLSIFDPPPFKV.TLTGGYLHIYESQLCCQLKFWLPIGCAA	149
mCRP1	. . . :	150
hCRP1	SSQGSYYFCSLSIFDPPPFQERNLSGGYLHIYESQLCCQLKLWLPVGCAA	150
hCRP1	FVVVCILGCILICWLTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTL	199
mCRP1	: .	200
	FVVVLLFGCILIIFWSKKKYGSSVHDPNSEYMFMAAVNTNKKSLAGVTS	200



APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIG. 14A

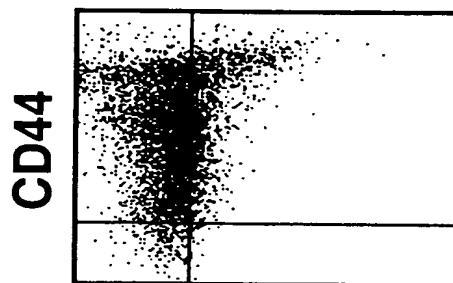


FIG. 14B

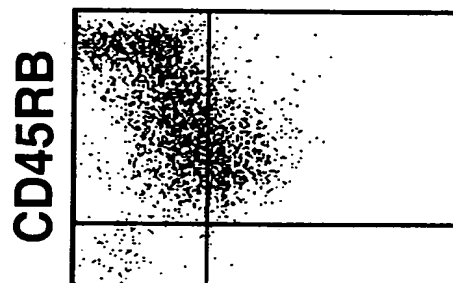
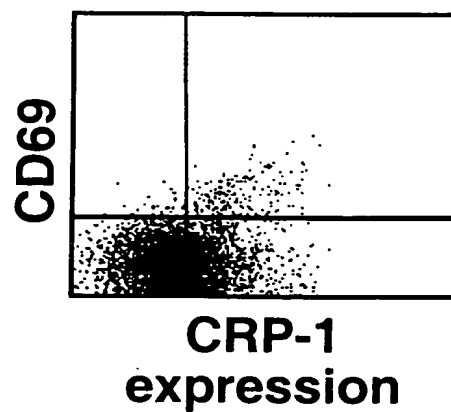


FIG. 14C





APPROVED	O.G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

FIG. 15A

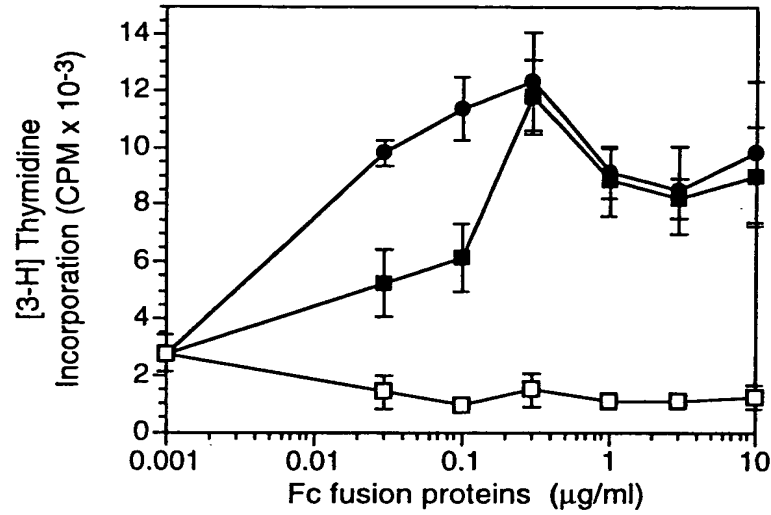
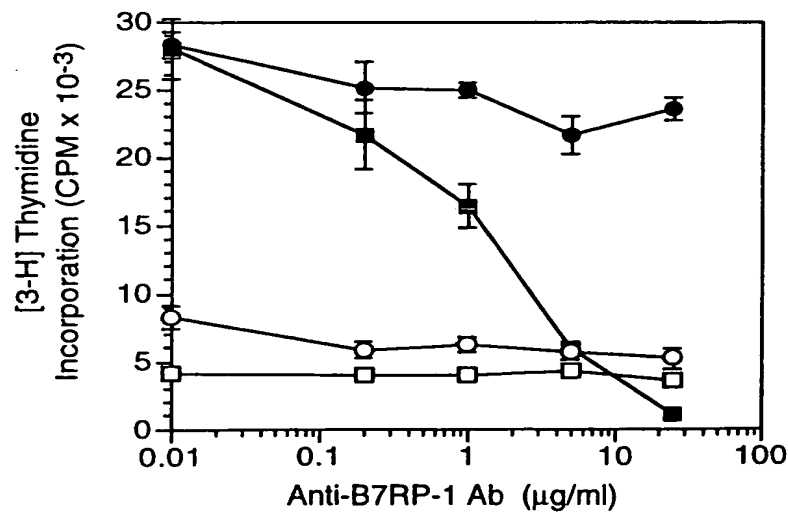


FIG. 15B





APPROVED	D.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIG. 16A

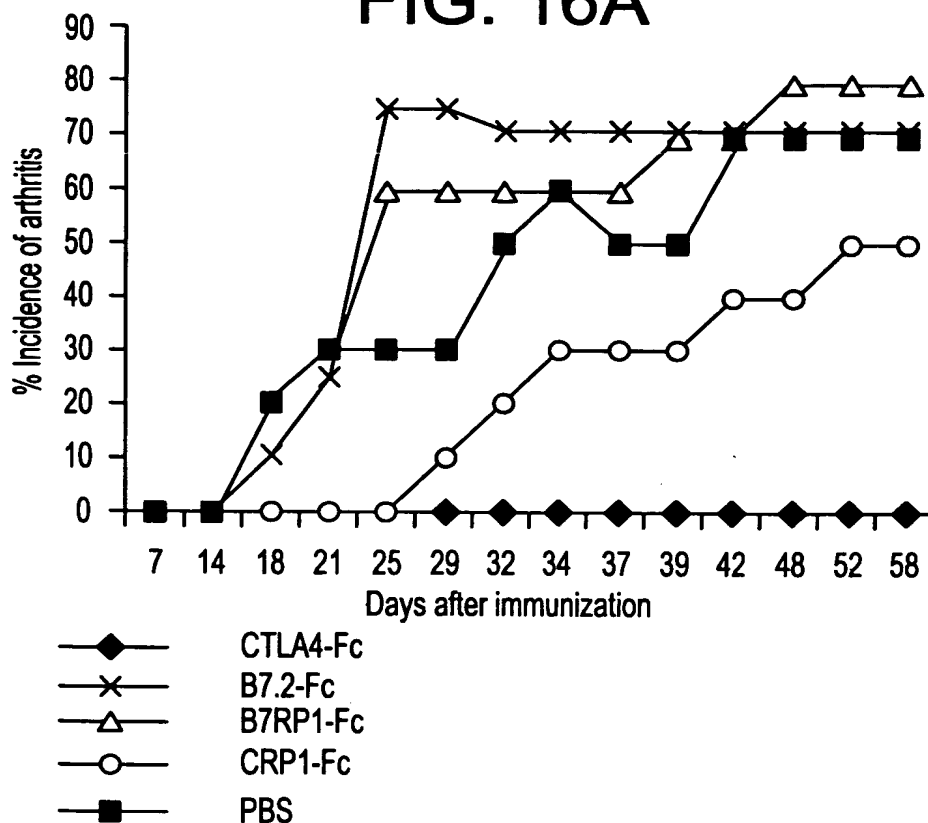


FIG. 16B

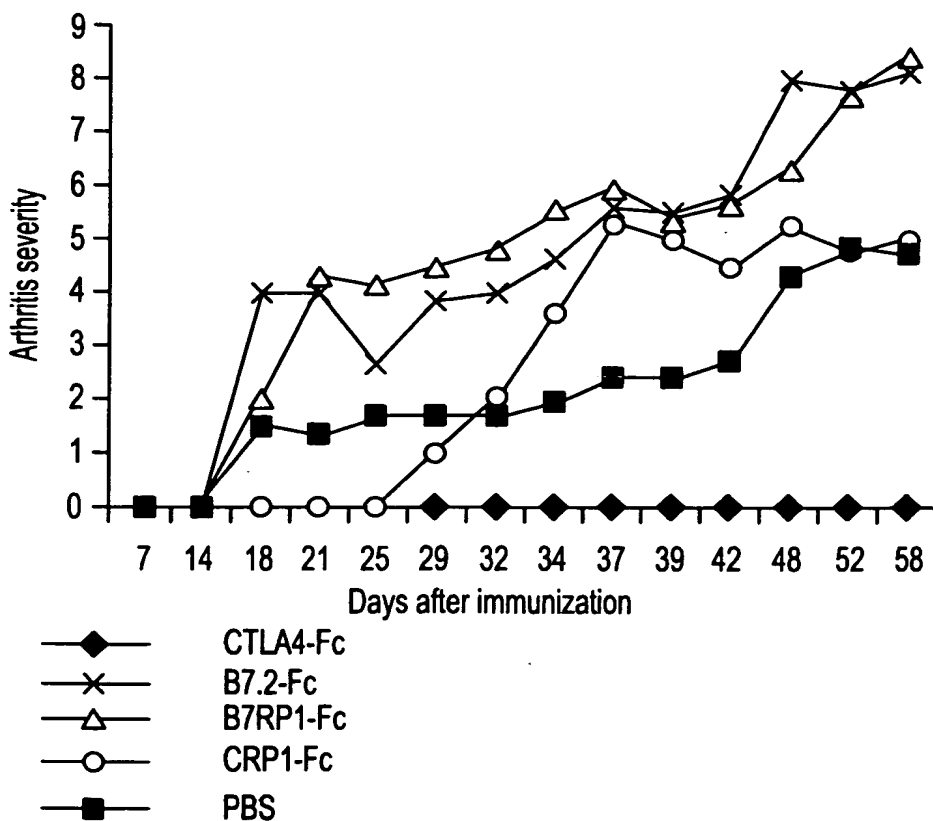
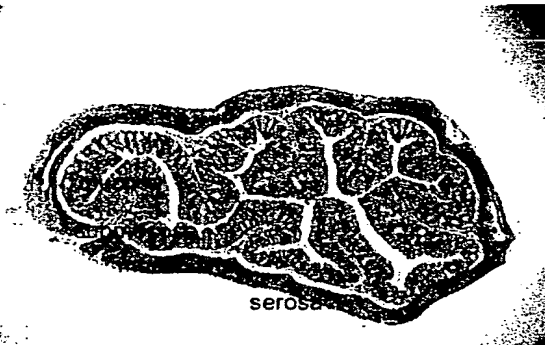




FIG. 17A



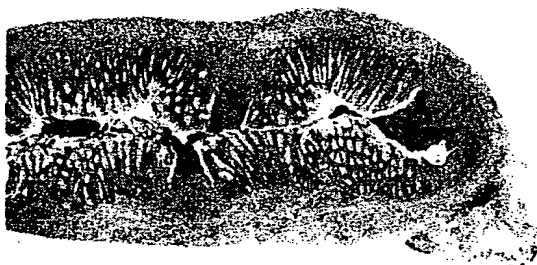
Control mouse#53F: Prox. colon 40X

FIG. 17B



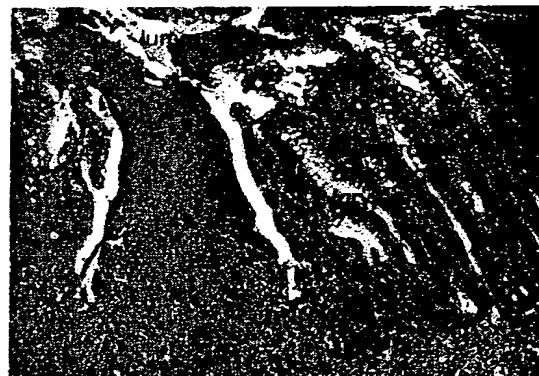
Mouse#111F: Prox. colon 40X

FIG. 17C



Mouse#111F: Prox. colon 20X

FIG. 17D



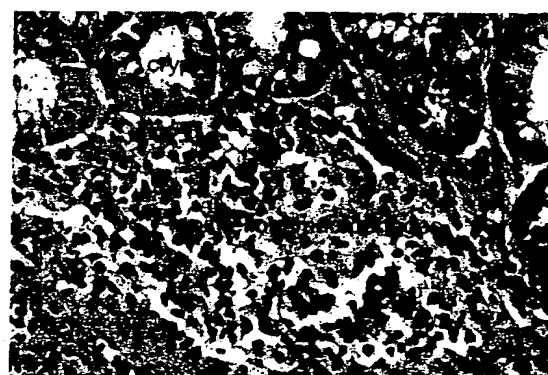
Mouse#111F: closeup of mucosa 100X

FIG. 17E



Mouse#112F: Giant cell, submucosa

FIG. 17F



Mouse#112F: epithelioid macrophages

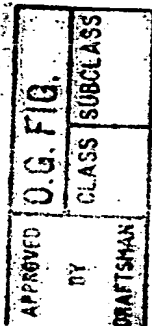
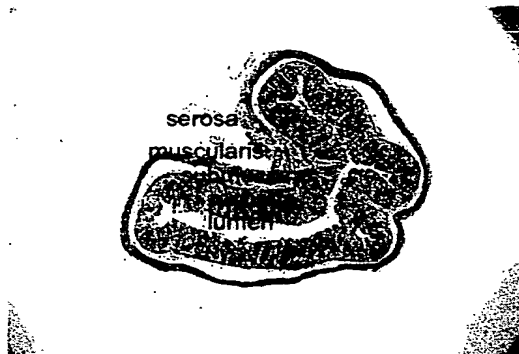




FIG. 18A



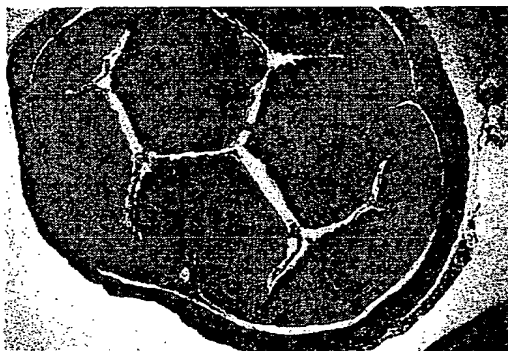
Control mouse#53F: Distal colon, 40X

FIG. 18B



Mouse#111F: Distal colitis, 40X

FIG. 18C



Mouse#55M: Distal colitis, 40X

FIG. 18D



Mouse#112F: Distal colon, 40X

FIG. 18E



Mouse#112: CD3+ T-cells, 40X

FIG. 18F



Mouse#112: closeup, 100X

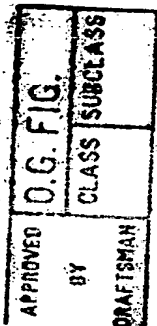




FIG. 19A



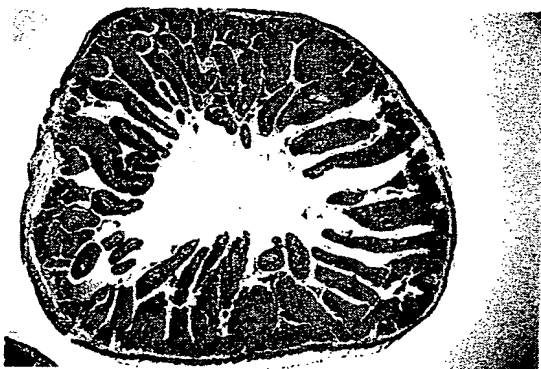
Control mouse#53F: duodenum, 40X

FIG. 19B



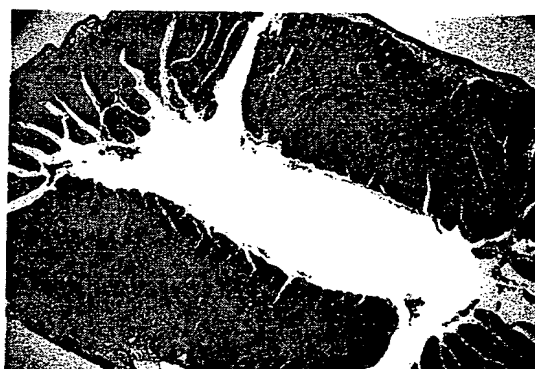
Mouse#51F: duodenum, 40X

FIG. 19C



Control mouse#53F: jejunum, 40X

FIG. 19D



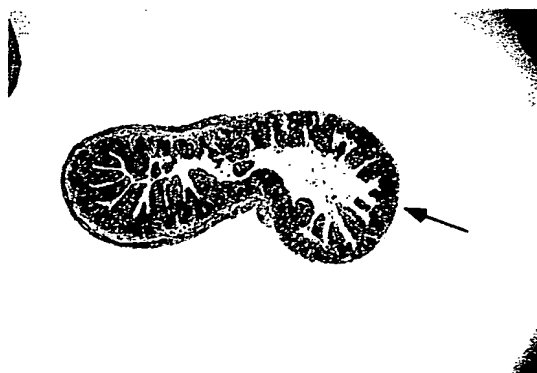
Mouse#51F: jejunal hyperplasia, 40X

FIG. 19E

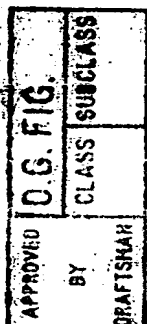


Mouse#53F: ileum, 40X

FIG. 19F



Mouse#231M: ileal atrophy, 40X





APPROVED	BY	DRAFTSMAN
O.G. FIG.		
CLASS SUBCLASS		

FIG. 20

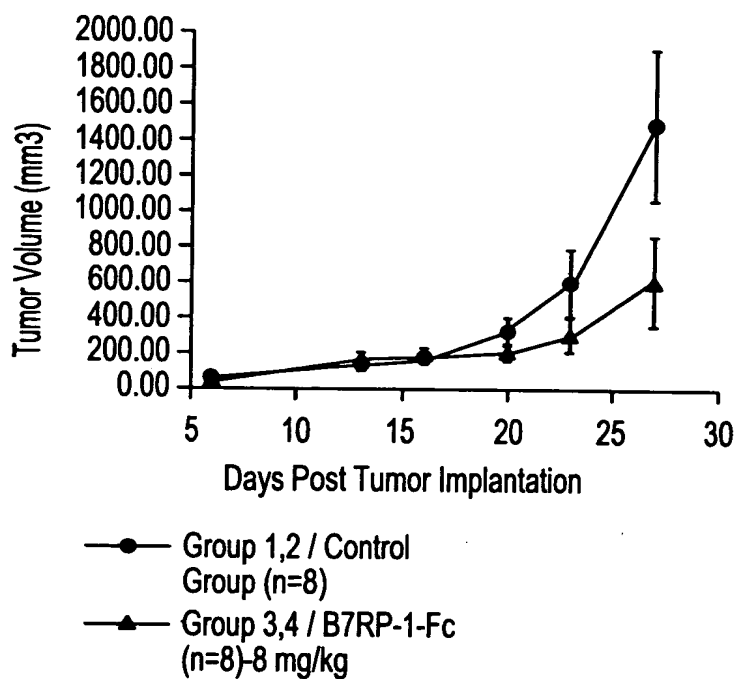




FIG. 21A

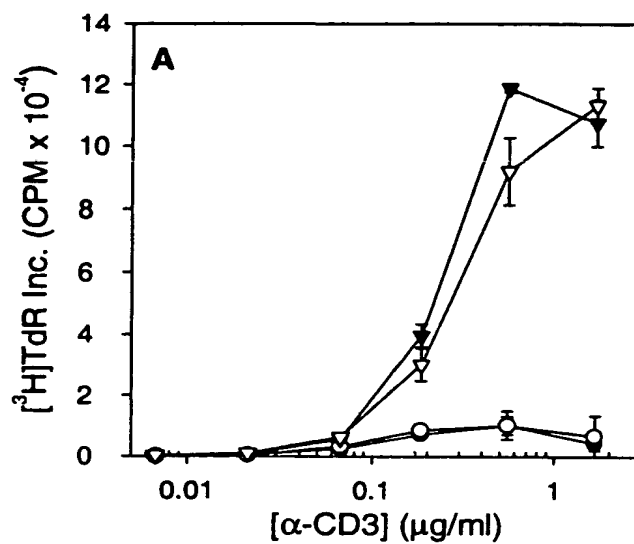


FIG. 21B

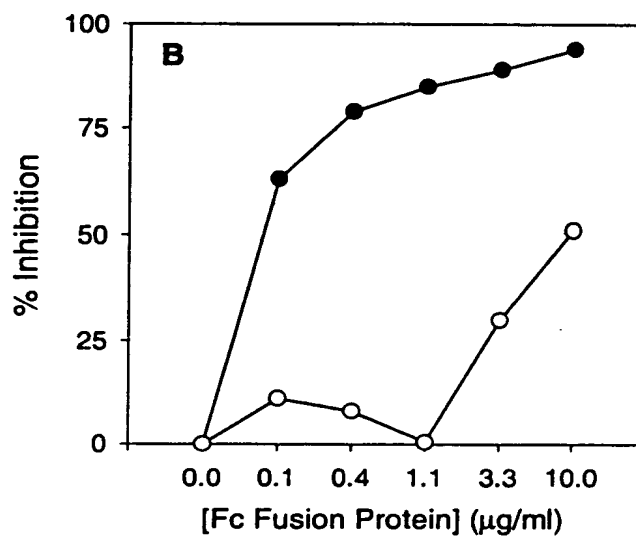
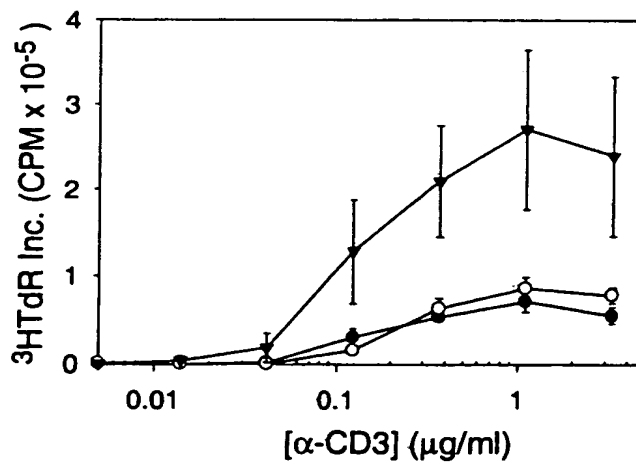


FIG. 21C





APPROVED	BY	DRAFTSMAN
O.G. FIG.		CLASS SUBCLASS

FIG. 21D

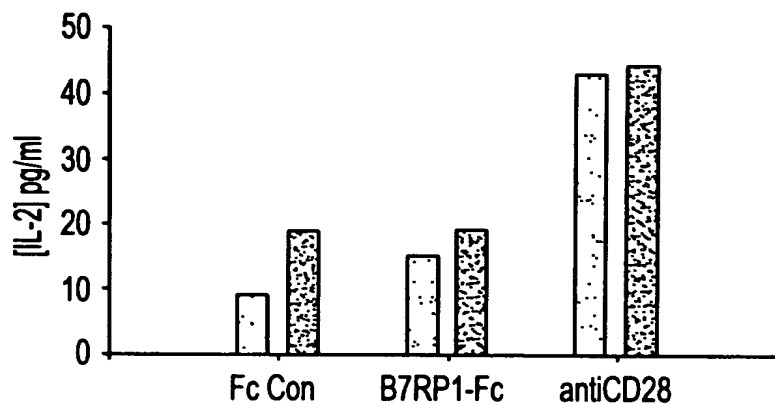


FIG. 21E

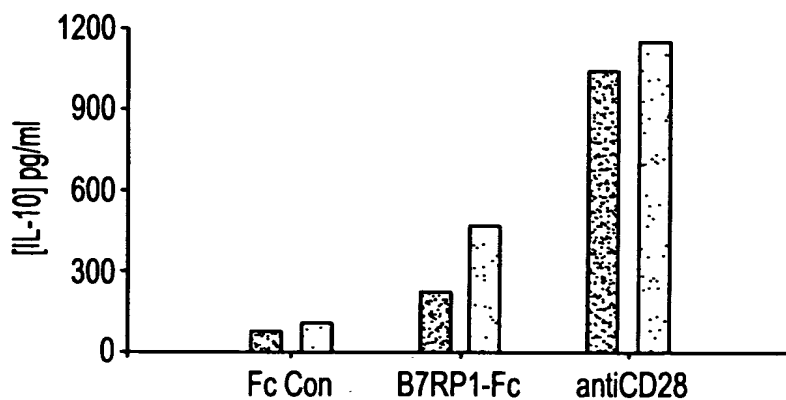
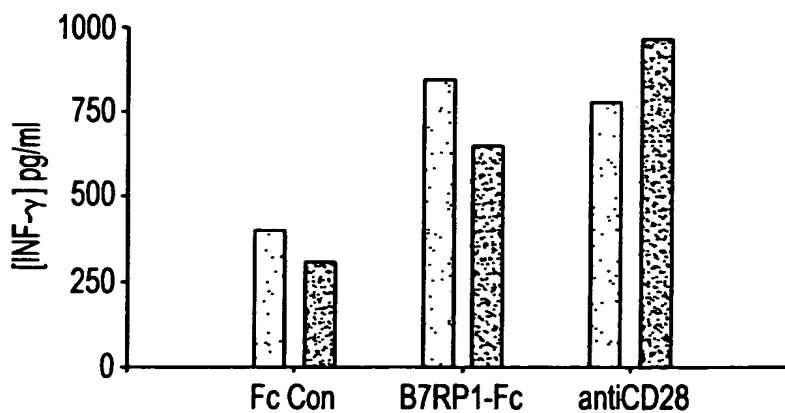


FIG. 21F



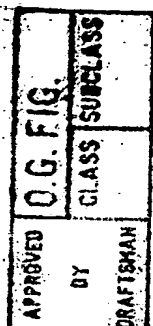


FIG. 22

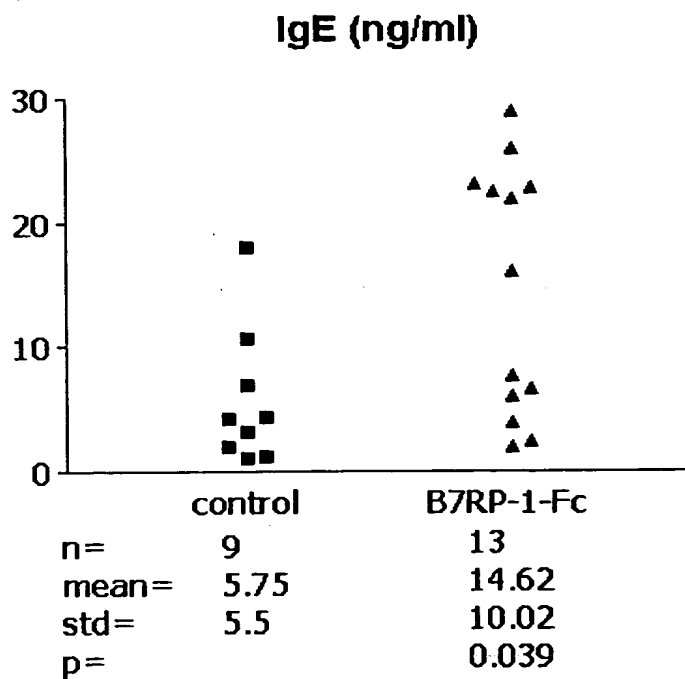




FIG. 23

